

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ruben, Steven M
- (ii) TITLE OF INVENTION: Apoptosis Inducing Molecule I
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Human Genome Sciences, Inc.
 - (B) STREET: 9410 Key West Avenue
 - (C) CITY: Rockville
 - (D) STATE: MD
 - (E) COUNTRY: US
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 13-MAR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kimball, Paul, C.
 - (B) REGISTRATION NUMBER: 34,610
 - (C) REFERENCE/DOCKET NUMBER: PF261
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (301) 309-8504
 - (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 52..894
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGCG GCTGCCTGGC TGA CTTACAG CAGTCAGACT CTGACAGGTT C ATG GCT
Met Ala

57

ATG ATG GAG GTC CAG GGG GGA CCC AGC CTG GGA CAG ACC TGC GTG CTG	105
Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys Val Leu	
5 10 15	
ATC GTG ATC TTC ACA GTG CTC CTG CAG TCT CTC TGT GTG GCT GTA ACT	153
Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala Val Thr	
20 25 30	
TAC GTG TAC TTT ACC AAC GAG CTG AAG CAG ATG CAG GAC AAG TAC TCC	201
Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser	
35 40 45 50	
AAA AGT GGC ATT GCT TGT TTC TTA AAA GAA GAT GAC AGT TAT TGG GAC	249
Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr Trp Asp	
55 60 65	
CCC AAT GAC GAA GAG AGT ATG AAC AGC CCC TGC TGG CAA GTC AAG TGG	297
Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val Lys Trp	
70 75 80	
CAA CTC CGT CAG CTC GTT AGA AAG ATG ATT TTG AGA ACC TCT GAG GAA	345
Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser Glu Glu	
85 90 95	
ACC ATT TCT ACA GTT CAA GAA AAG CAA CAA AAT ATT TCT CCC CTA GTG	393
Thr Ile Ser Thr Val Gln Lys Gln Gln Asn Ile Ser Pro Leu Val	
100 105 110	
AGA GAA AGA GGT CCT CAG AGA GTA GCA GCT CAC ATA ACT GGG ACC AGA	441
Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg	
115 120 125 130	
GGA AGA AGC AAC ACA TTG TCT TCT CCA AAC TCC AAG AAT GAA AAG GCT	489
Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala	
135 140 145	
CTG GGC CGC AAA ATA AAC TCC TGG GAA TCA TCA AGG AGT GGG CAT TCA	537
Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser	
150 155 160	
TTC CTG AGC AAC TTG CAC TTG AGG AAT GGT GAA CTG GTC ATC CAT GAA	585
Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu	
165 170 175	
AAA GGG TTT TAC TAC ATC TAT TCC CAA ACA TAC TTT CGA TTT CAG GAG	633
Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu	
180 185 190	
GAA ATA AAA GAA AAC ACA AAG AAC GAC AAA CAA ATG GTC CAA TAT ATT	681
Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile	
195 200 205 210	
TAC AAA TAC ACA AGT TAT CCT GAC CCT ATA TTG TTG ATG AAA AGT GCT	729
Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala	
215 220 225	
AGA AAT AGT TGT TGG TCT AAA GAT GCA GAA TAT GGA CTC TAT TCC ATC	777
Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile	
230 235 240	

TAT CAA GGG GGA ATA TTT GAG CTT AAG GAA AAT GAC AGA ATT TTT GTT	825
Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val	
245 250 255	
TCT GTA ACA AAT GAG CAC TTG ATA GAC ATG GAC CAT GAA GCC AGT TTT	873
Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe	
260 265 270	
TTC GGG GCC TTT TTA GTT GGC TAACTGACCT GGAAAGAAAA AGCAATAACC	924
Phe Gly Ala Phe Leu Val Gly	
275 280	
TCAAAGTGAC TATTCAGTTT TCAGGATGAT ACACATATGAA GATGTTTCAA AAAATCTGAC	984
CAAAACAAAC AAACAGAAAA CAGAAAACAA AAAAACCTCT ATGCAATCTG AGTAGAGCAG	1044
CCACAACCAA AAAATTCTAC AACACACACT GTTCTGAAAG TGACTIONT ATCCCAAGAA	1104
AATGAAATTG CTGAAAGATC TTTTCAGGACT CTACCTCATA TCAGTTTGCT AGCAGAAAATC	1164
TAGAAGACTG TCAGCTTCCA AACATTAATG CAATGGTTAA CATCTTCTGT CTTTATAATC	1224
TACTCCTTGT AAAGACTGTA GAAGAAAGCG CAACAATCCA TCTCTCAAGT AGTGTATCAC	1284
AGTAGTAGCC TCCAGGTTTC CTTAAGGGAC AACATCCTTA AGTCAAAGA GAGAAGAGGC	1344
ACCACTAAAA GATCGCAGTT TGCCTGGTGC AGTGGCTCAC ACCTGTAATC CCAACATTTT	1404
GGGAACCCAA GGTGGGTAGA TCACGAGATC AAGAGATCAA GACCATAGTG ACCAACATAG	1464
TGAAACCCCA TCTCTACTGA AAGTGCAAAA ATTAGCTGGG TGTGTTGGCA CATGCCTGTA	1524
GTCCAGCTA CTTGAGAGGC TGAGGCAGGA GAATCGTTTG AACCCGGGAG GCAGAGGTTG	1584
CAGTGTGGTG AGATCATGCC ACTACACTCC AGCCTGGCGA CAGAGCGAGA CTTGGTTTC	1643

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
1 5 10 15
Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
20 25 30
Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45
Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp	Asp	Pro	Asn	Asp	Glu	Glu	Ser	Met	Asn	Ser	Pro	Cys	Trp	Gln	Val	65	70	75	80
Lys	Trp	Gln	Leu	Arg	Gln	Leu	Val	Arg	Lys	Met	Ile	Leu	Arg	Thr	Ser	85	90	95	
Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro	100	105	110	
Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	115	120	125	
Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	130	135	140	
Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	145	150	155	160
His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	165	170	175	
His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	180	185	190	
Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	195	200	205	
Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	210	215	220	
Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	225	230	235	240
Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile	245	250	255	
Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala	260	265	270	
Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly	275	280									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val	Asp	Ser	Ser	Ala	Ser	Ser	Pro	Trp	Ala	Pro	Pro	Gly	Thr	Val	Leu	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Pro Cys Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro
 20 25 30
 Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro
 35 40 45
 Leu Pro Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser
 50 55 60
 Thr Gly Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu
 65 70 75 80
 Val Gly Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu
 85 90 95
 Leu Ala Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser
 100 105 110
 Leu Glu Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu
 115 120 125
 Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met
 130 135 140
 Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val
 145 150 155 160
 Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe
 165 170 175
 Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro
 180 185 190
 Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
 195 200 205
 Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met
 210 215 220
 Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala
 225 230 235 240
 Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu
 245 250 255
 Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gln Gln Pro Met Asn Tyr Pro Cys Pro Gln Ile Phe Trp Val Asp
1 5 10 15
Ser Ser Ala Thr Ser Ser Trp Ala Pro Pro Gly Ser Val Phe Pro Cys
20 25 30
Pro Ser Cys Gly Pro Arg Gly Pro Asp Gln Arg Arg Pro Pro Pro Pro
35 40 45
Pro Pro Pro Val Ser Pro Leu Pro Pro Pro Ser Gln Pro Leu Pro Leu
50 55 60
Pro Pro Leu Thr Pro Leu Lys Lys Lys Asp His Asn Thr Asn Leu Trp
65 70 75 80
Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly
85 90 95
Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu
100 105 110
Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln
115 120 125
Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val
130 135 140
Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp
145 150 155 160
Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys
165 170 175
Gly Gly Leu Val Ile His Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys
180 185 190
Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys
195 200 205
Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu
210 215 220
Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser
225 230 235 240
Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr
245 250 255
Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr
260 265 270
Phe Phe Gly Leu Tyr Lys Leu
275

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1          5          10          15
Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20          25          30
Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35          40          45
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Ser Pro
50          55          60
Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65          70          75          80
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
85          90          95
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
100         105         110
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
115         120         125
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
130         135         140
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145         150         155         160
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
165         170         175
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
180         185         190
Pro Ile Tyr Leu Gly Cys Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
195         200         205
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
210         215         220
Gln Val Tyr Phe Gly Ile Ile Ala Leu
225         230

```

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
1          5          10          15
Leu His Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
20          25          30
Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
35          40          45
Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
50          55          60
Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
65          70          75          80
Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
85          90          95
Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
100         105         110
Val Val Phe Ser Cys Lys Ala Tyr Ser Pro Lys Ala Pro Ser Ser Pro
115         120         125
Leu Tyr Leu Ala His Glu Val Cys Leu Phe Ser Ser Gln Tyr Pro Phe
130         135         140
His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
145         150         155         160
Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
165         170         175
Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
180         185         190
Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
195         200         205

```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCGGGAT CCATGGCTAT GATGGAGGTC CAG

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGCGTCTA GAGCTTAGGC AACTAAAAAG GCC

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGCGCGGAT CCATCATGGC TATGATGGAG GTCC

34

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGCGTCTA GAGCTTAGCC AACTAAAAAG GCC

33